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<120>    INSECT RESISTANT COTTON PLANTS AND METHODS OF DETECTING THE SAME
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<213>    Artificial Sequence
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<223>    COT202 nucleotide motif

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aacaaacaca aaatcttttc accagt                                          26


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<400>    2
ttcccgcctt cagattttct gcaaca                                          26


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<400>    3
ggtgtccatc gggtagtcca taa                                          23


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<400>    4
tctatgttac tagatcggga attg                                          24


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gatcggggtc aggaaggtct                                                                    .20


<210>   6
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<400>   6
cagcatcatg aacgagcact                                                                    20


<210>   7
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<400>   7
gacaaggaca gcttgagcga ggtgatctac ggcgacatgg acaagctgct gtgtccggac          60

cagagcgagc aaatctacta caccaacaac atcgtgttcc cgaacgagta cgtgatcacc          120

aagatcgact tcaccaagaa gatgaagacc ctgcgctacg aggtgaccgc caacttctac          180

gacagcagca ccggcgagat cgacctgaac aagaagaagg tggagagcag cgaggccgag          240

taccgcaccc tgagcgcgaa cgacgacggc gtctacatgc cactgggcgt                      290


<210>   8
<211>   4382
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<400>   8
gatttggagc caagtctcat aaacgccatt gtggaagaaa gtcttgagtt ggtggtaatg          60

taacagagta gtaagaacag agaagagaga gagtgtgaga tacatgaatt gtcgggcaac          120

aaaaatcctg aacatcttat tttagcaaag agaaagagtt ccgagtctgt agcagaagag          180

tgaggagaaa tttaagctct tggacttgtg aattgttccg cctcttgaat acttcttcaa          240

tcctcatata ttcttcttct atgttacctg aaaaccggca tttaatctcg cgggtttatt          300

ccggttcaac attttttttg ttttgagtta ttatctgggc ttaataacgc aggcctgaaa          360

taaattcaag gcccaactgt tttttttttt aagaagttgc tgttaaaaaa aaaaaaaggg          420

aattaacaac aacaacaaaa aaagataaag aaaataataa caattacttt aattgtagac          480

taaaaaaaca tagattttat catgaaaaaa agagaaaaga aataaaaact tggatcaaaa          540
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aaaaacatac agatcttcta attattaact tttcttaaaa attaggtcct ttttcccaac    600

aattaggttt agagttttgg aattaaacca aaaagattgt tctaaaaaat actcaaattt    660

ggtagataag tttccttatt ttaattagtc aatggtagat acttttttt cttttctta      720

ttagagtaga ttagaatctt ttatgccaag tattgataaa ttaaatcaag aagataaact    780

atcataatca acatgaaatt aaaagaaaaa tctcatatat agtattagta ttctctatat    840

atattatgat tgcttattct taatgggttg ggttaaccaa gacatagtct taatggaaag    900

aatctttttt gaacttttc cttattgatt aaattcttct atagaaaaga agaaattat      960

ttgaggaaaa gtatatacaa aaagaaaaat agaaaaatgt cagtgaagca gatgtaatgg   1020

atgacctaat ccaaccacca ccataggatg tttctacttg agtcggtctt ttaaaaacgc   1080

acggtggaaa atatgacacg tatcatatga ttccttcctt tagtttcgtg ataataatcc   1140

tcaactgata tcttcctttt tttgttttgg ctaaagatat tttattctca ttaatagaaa   1200

agacggtttt gggcttttgg tttgcgatat aaagaagacc ttcgtgtgga agataataat   1260

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aatctctcgc gactctctct ttcaaggtat attttctgat tcttttgtt tttgattcgt     1380

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aatattgttc gtttcgtcaa tccagcttct aaattttgtc ctgattacta agatatcgat   1500

tcgtagtgtt tacatctgtg taatttcttg cttgattgtg aaattaggat tttcaaggac   1560

gatctattca atttttgtgt tttctttgtt cgattctctc tgttttaggt ttcttatgtt   1620

tagatccgtt tctctttggt gttgtttga tttctcttac ggcttttgat ttggtatatg     1680

ttcgctgatt ggtttctact tgttctattg ttttatttca ggtggatcca ccatgaacaa   1740

gaacaacacc aagctgagca cccgcgccct gccgagcttc atcgactact caacggcat    1800

ctacggcttc gccaccggca tcaaggacat catgaacatg atcttcaaga ccgacaccgg   1860

cggcgacctg accctggacg agatcctgaa gaaccagcag ctgctgaacg acatcagcgg   1920

caagctggac ggcgtgaacg gcagcctgaa cgacctgatc gcccagggca acctgaacac   1980

cgagctgagc aaggagatcc ttaagatcgc caacgagcag aaccaggtgc tgaacgacgt   2040

gaacaacaag ctggacgcca tcaacaccat gctgcgcgtg tacctgccga gatcaccag     2100

catgctgagc gacgtgatga agcagaacta cgccctgagc ctgcagatcg agtacctgag   2160

caagcagctg caggagatca gcgacaagct ggacatcatc aacgtgaacg tcctgatcaa   2220

cagcaccctg accgagatca ccccggccta ccagcgcatc aagtacgtga acgagaagtt   2280

cgaagagctg accttcgcca ccgagaccag cagcaaggtg aagaaggacg cagcccggc     2340
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cgacatcctg gacgagctga ccgagctgac cgagctggcg aagagcgtga ccaagaacga   2400

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gttcggccgc agcgccctga agaccgccag cgagctgatc accaaggaga acgtgaagac   2520

cagcggcagc gaggtgggca acgtgtacaa cttcctgatc gtgctgaccg ccctgcaggc   2580

ccaggccttc ctgaccctga ccacctgtcg caagctgctg ggcctggccg acatcgacta   2640

caccagcatc atgaacgagc acttgaacaa ggagaaggag gagttccgcg tgaacatcct   2700

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ccagagcgag caaatctact acaccaacaa catcgtgttc ccgaacgagt acgtgatcac   3000

caagatcgac ttcaccaaga agatgaagac cctgcgctac gaggtgaccg ccaacttcta   3060

cgacagcagc accggcgaga tcgacctgaa caagaagaag gtggagagca gcgaggccga   3120

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gaccttcctg accccgatca cggctttgg cctgcaggcc gacgagaaca gccgcctgat   3240

caccctgacc tgtaagagct acctgcgcga gctgctgcta gccaccgacc tgagcaacaa   3300

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catcgaggag gacaacctgg agccgtggaa ggccaacaac aagaacgcct acgtggacca   3420

caccggcggc gtgaacggca ccaaggccct gtacgtgcac aaggacggcg gcatcagcca   3480

gttcatcggc gacaagctga gccgaagac cgagtacgtg atccagtaca ccgtgaaggg   3540

caagccatcg attcacctga aggacgagaa caccggctac atccactacg aggacaccaa   3600

caacaacctg gaggactacc agaccatcaa caagcgcttc accaccggca ccgacctgaa   3660

gggcgtgtac ctgatcctga agagccagaa cggcgacgag gcctggggcg acaacttcat   3720

catcctggag atcagcccga gcgagaagct gctgagcccg gagctgatca acaccaacaa   3780

ctggaccagc accggcagca ccaacatcag cggcaacacc ctgaccctgt accagggcgg   3840

ccgcggcatc ctgaagcaga acctgcagct ggacagcttc agcacctacc gcgtgtactt   3900

cagcgtgagc ggcgacgcca acgtgcgcat ccgcaactcc cgcgaggtgc tgttcgagaa   3960

gaggtacatg agcggcgcca aggacgtgag cgagatgttc accaccaagt tcgagaagga   4020

caacttctac atcgagctga ccagggcaa caacctgtac ggcggcccga tcgtgcactt   4080

ctacgacgtg agcatcaagt aggagctcta gatccccgga atttccccga tcgttcaaac   4140
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atttggcaat aaagtttctt aagattgaat cctgttgccg gtcttgcgat gattatcata   4200

taatttctgt tgaattacgt taagcatgta ataattaaca tgtaatgcat gacgttattt   4260

atgagatggg tttttatgat tagagtcccg caattataca tttaatacgc gatagaaaac   4320

aaaatatagc gcgcaaacta ggataaatta tcgcgcgcgg tgtcatctat gttactagat   4380

cg                                                                  4382
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<210>   9
<211>   789
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<213>   Artificial Sequence
<220>
<223>   VIP3A protein motif

<400>   9
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Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp
                20                  25                  30

Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu
            35                  40                  45

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys
        50                  55                  60

Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn
65                  70                  75                  80

Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln
                85                  90                  95

Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr
            100                 105                 110

Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val
            115                 120                 125

Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys
    130                 135                 140

Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val
145                 150                 155                 160

Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile
                165                 170                 175

Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr
            180                 185                 190

Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu Asp Glu
        195                 200                 205

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Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val
    210             215             220

Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly
225             230             235             240

Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile
            245             250             255

Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
            260             265             270

Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Gln Ala Phe Leu Thr
            275             280             285

Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr
    290             295             300

Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val
305             310             315             320

Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala
            325             330             335

Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys
            340             345             350

Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr
            355             360             365

Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp
    370             375             380

Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu
385             390             395             400

Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe
            405             410             415

Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys
            420             425             430

Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
    435             440             445

Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr
    450             455             460

Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val
465             470             475             480

Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala
            485             490             495

Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg
            500             505             510

Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile
            515             520             525
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Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile
    530                 535             540

Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr
545             550             555                 560

Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His
            565             570                 575

Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys
        580             585             590

Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His
        595             600             605

Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn
    610             615             620

Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr Gly Thr
625             630             635                 640

Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu
            645             650             655

Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys
            660             665             670

Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly
        675             680             685

Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg
    690             695             700

Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg
705             710             715                 720

Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser
            725             730             735

Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val
            740             745             750

Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr Ile Glu
            755             760             765

Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro Ile Val His Phe Tyr
    770             775             780

Asp Val Ser Ile Lys
785
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<210>   10
<211>   20
<212>   DNA
<213>   Artificial Sequence
<220>
<223>   COT202 nucleotide motif
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ggtccctgga tacggtgtca                                          20


<210>  11
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<223>  COT202 nucleotide motif

<400>  11
ttgagggttg gatcctttgc                                          20


<210>  12
<211>  26
<212>  DNA
<213>  Artificial Sequence
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<223>  COT202 nucleotide motif

<220>
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<222>  (1)..(1)
<223>  VIC label at 5' end

<220>
<221>  modified_base
<222>  (26)..(26)
<223>  TAMRA label at 3' end

<400>  12
caccaacatc atcaatggtg gcatcg                                   26


<210>  13
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<212>  DNA
<213>  Artificial Sequence
<220>
<223>  COT202 nucleotide motif

<400>  13
ggaatgtggc gaatggtgat                                          20


<210>  14
<211>  18
<212>  DNA
<213>  Artificial Sequence
<220>
<223>  COT202 nucleotide motif

<400>  14
tgtcgtttcc cgccttca                                            18


<210>  15
<211>  29
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<212>   DNA
<213>   Artificial Sequence
<220>
<223>   COT202 nucleotide motif

<220>
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<222>   (1)..(1)
<223>   FAM label at 5' end

<220>
<221>   modified_base
<222>   (29)..(29)
<223>   TAMRA label at 3' end

<400>   15
caaattgccc atttcattca tccaaaagc                                              29


<210>   16
<211>   23
<212>   DNA
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<223>   COT202 nucleotide motif

<400>   16
ggtgtccatc gggtagtcca taa                                                    23


<210>   17
<211>   24
<212>   DNA
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<223>   COT202 nucleotide motif

<400>   17
tgagtaggag atgtaagttg gcgc                                                   24


<210>   18
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<212>   DNA
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<223>   COT202 nucleotide motif

<400>   18
tctatgttac tagatcggga attg                                                   24
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